FIGURE 1A

```
  1  GNTCTAGAAN TAGTGGATCC CCCGGGGCTG CAGGAATTCC GGAAGGGCTC TGGTGGGGCT GAGCGGCTCTG
     CNAGATCTTN ATCACCTAGG GGGCCCCGAC GTCCTTAAGG CCTTCCCGAG ACCACCCCGA CTCGCCGAGAC

101  CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CGGGGTGGTC CGGGGTGAAG AGCCAGGCAG CCGGGGCGAC
     GTCCTTCGTC CAGGCGCACC CGCGACCCCC GCCCCACCAG GCCCCACTTC TCGGTCCGTC GGCCCCGCTG

201  TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG GTCATGGGGC CCCCCCATTC TGGGCCGGGG TCGGGCCCT
     AAACCCCCTC AACCACGGGG CGGGGGGTCC CAGTACCCCG GGGGGGTAAG ACCCGGCCCC AGCCCGGGA
  1                                  MetGlyP    roProHisSe rGlyProGly GlyValArgv alGlyAlaLe uLeuLeuLeu

301  GGGGTTTTGG GGCTGGTGTC TCTACTGGAA CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC
     CCCCAAAACC CCGAGTCAGC AGATGACCTT GAGCCGCTTA TTCTCCAAGG TCCGTCTCCC ACCAATACAC GACATGGGAG
 20  lyLeuValSe rGlyLeuProV alTyrTrpAs nSerAlaAsn LysArgPheG lnAlaGluGl yGlyTyrVal LeuTyrProGln

401  AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCG GCCTCCTAATTA TGAGTTCTAC AAGTGTACC TGGTAGGGG
     TCTAGCCCCT GGCCGATCTG GACGAGACGG GGGCCCGGGC CGGAGGATTAAT ACTCAAGATG TTCACATGG ACCATCCCC
 54  IleGlyAs  pArgLeuAsp LeuLeuCysP roArgAlaAr gProProGly ProHisSerS erProAsnTy rLysLeuTyrL euValGlyGly

501  TGCTCAGGGC CGGCGCTGTG AGGCACCCCC CTCCTTCTCA CTTGTGATCG CCCAGACCTG GTTCCAGGAG
     ACGAGTCCCG GCCGCGACAC TCCGTGGGGG GAGGAAGAGT GAACACTAGC GGGTCTGGAC CAAGGTCCTC
 87  AlaGlnGly ArgArgCysG luAlaProAr oAlaProAsn LeuLeuLeuT hrCysAspAr gProAspLeu AspLeuArgP heThrIleLy sPheGlnGlu

601  TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA CATCATTGCC ACATCGGATG AGCCTGCAGG
     ATATCGGGAT TAGAGACCCC GGTGCTCAAG GCGAGCGTGG TGCTAATGAT GTAGTAACGG TGTAGCCTAC TCGGACGTCC
120  TyrSerProA snLeuTrpGl yHisGluPhe ArgSerHisH isAspTyrTy rIleIleAla ThrSerAspG lyThrArgGl uGlyLeuGlu SerLeuGlnGly

701  GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA AGTCCCCGAG GGACCCGGATG CCCCCGAAAA
     CTCCACACAC GGATTGGTCT CCGTACTTCC ACGAAGAGGC TCACCCTGTT TCAGGGGCTC CCTGGGGCCT CCGGGGCTTTT
154  GlyValCy  sLeuThrArg GlyMetLysV alGlyGlyGln SerProArgG lProArgLys ProValSerG luMetProMet

801  GGAAAGAGAC CGAGGGGCAG CCCCACCAGCT GGAGCCTGGG AAGGAGAACC TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC
     CCTTTCTCTG GCTCCCCGTC GGGGTGTCGGA CCTCGGACCC TTCCTCTTGG ACGGTCCACT GGGGTGGTCG TTACGTTGGA GGGCCCCACG
187  GluArgAsp ArgGlyAlaA laHisSerLe uGluProGly LysGluAsnL euProThrSer AsnAlaThrS erArgGlyAl aGluGlyPro

901  CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGTGG CTGGGCTCTTG GGTGGTCCATG TGTTGGCGGA
     GACGGGGGAG GGTCGTACGG ACGTCACCGA CCCCGTCGTC CCCCCGACCG GACCCGAGAAC CCACCGGGTAC ACAACGCCCT
220  LeuProProP roSerMetPr oAlaValAla GlyAlaAlaG lyAlaLeuAl aLeuLeuVal AlaGlyAlaLal yGlyAlaMet CysTrpArgArg

1001 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC GAGAGCCGTCC ACCCTGGTCC TGGCTCCTTC GGTCTCTGGG GGTTCTTTTG
     CTGCCGCCCG GTTCGGAAGC CTCTCAGCGG CTCTCAGCGGG TGGGACCAGG ACCGAGGAAG CCAGAGACCC CCAGAGACCC
254  ArgArgAl  aLysProSer GluSerArgH isProGlyPr oGlySerPhe GlyArgGlyG lySerLeuGl yLeuGlyGly GlyGlyGlyPro

1101 GGAGGCTGAG CCTGGGGGAGC TAGGGATAGC TCTGCGGGGT GGCGGGGGGC CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGACTATGGG
     CCTCCGACTC GGACCCCCTG ATCCCTATCG ATCCCTATCG AGCGCCCCCA CCGCCCCCCG GTCTAGGGGG GAAGACGGGG GTGATACTCT TCCACTCACC ACTGATACCC
287  GluAlaGlu ProGlyGlyL euGlyIleAl aLeuArgGly HisTyrGluL oPheCysPr  oAspProPr  GlnValSerGl ysValSerGl yAspTyrGly
```

FIGURE 1B

```
1201 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTACTACACA TCGATTTCTG TGTTGGAGTG GCCCATATTG CATACGATAC
     GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GATGATGTGT AGCTAAAGAC ACAACCTCAC CGGGTATAAC GTATGCTATG
320  HisProValT yrIleValGl nAspGlyPro roProGlnSerP eTyrTyrThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln

1301 AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACTAC ATTCTTATTT CCTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
     TTGACAAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTC AATAATGCTG TAGCTGAACG GCCTACTGAA GTAAATCGAA
354  LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe

1401 TACCACCCTG AACCCATCCA TGCAGGCCTG CAGAGCACAG ATGGGGGAAT TCCGAATCAG ATGGTGTTTC TGGGGGGACA GGATCCTGGG TACGGCTCTG
     ATGGTGGGAC TTGGGTAGGT ACGTCCGGAC GTCTCGTGTC TACCCCCTTA AGGCTTAGTC TACCACAAAG ACCCCCCTGT CCTAGGACCC ATGCCGAGAC
387  ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe rgIleLeuGl yThrAlaLeu

1501 TTTGTGCTTG TGCTTATTCT TCTTCTTGGG AGGCTGAATA TGCATCAGAC CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
     AAACACGAAC ACGAATAAGA AGAAGAACCC TCCGACTTAT ACGTAGTCTG GGTCACACCT CCGCCTTCGG CCGGTCGTAC
420  PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu ArgGlnArgA laSerValGl uAlaGluAla GlyGlnHisGly

1601 GTCCCCTGTG ATAGGATTGA AAGAGCTACT GAGAGAGCG GGCTTCTCAA TTATCATGGG AACCAGGCAG ATCAATCATC
     CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTCTCGC CCGAAGAGTT CTCCGACGAC TTGGTCCGTC TAGTTAGTAG
454  ProLeu

1701 CCTGGCAGT CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG
     GGACCGTCCA GTCCGTCCTT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGTCTTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC

1801 TGCTGCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTGA TATCAAGCTT ATCGATACCG TCGACCT
     ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAACCT ATAGTTCGAA TAGCTATGGC AGCTGGA
```

FIGURE 2A

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1    GNTCTAGAAN TACTCGATCC CCCCGGGCTG CAGGAATTCC GACCCCCCCT GGAAGGGCTC TGGTGGGGCT GAGGGCTCTG CCCGGGGGGC GCGGGCCACAG
     CNAGATCTTN ATCACCTAGG CGGGCCCGAC GTCCTTAAGG CTGCCGGGGA CCTTCCCGAG ACCACCCCGA CCAAGCCCGA CTCGCGGAGAC GGGCGCCCCG CGCCGGCCGTC

101  CAGGAAGCAG GTCCCCCTGG GCGCTGGGGG CATCAGCTAC CGGGGCTGTC CGGGCTGAAG AGCCAGGCAG AGCCTGGCCCTG CACCCCCGGG GGTGGGCGAC
     GTCCTTCGTC CAGGCGCACC CKCGACXCCC GTAGTCGATG GCCCCACCAG CCCCGACTTC TCGGTCCGTC GGCTCCGTCG GGTGGGGCCC CCACCCCCGTC

201  TTTGGGGGAC TTGGTCCCCC CCCCCTGCCC CCTTCGGGGG GTCATGGGGC CCCCCATTC TGGGCCCGGGC TCGGGCCCCT CCTGCTGCTG
     AAACCCCCTC AACCACGGGG CGGGGGGTCC GGAACCGGCC CAGTACCCCG ACCCGCCCC GGGGGTAAG ACCCGCCCCC AGCCCCCGGA CCAGGACGAC
     1                                           MetGlyP    roProllsse rGlyProGly GlyValArgv aLeuLeuLeu uLeuLeuLeu

301  GGGGTTTTGG GGCTGGTGTC TCGGCTCAGC CTGGAGCCTG TCTACTGGAA CTCGGGCGAAT AAGAGGTTCC AGGCAGAGG TGGTTATGTG CCGTACCCTC
     CCCCAAAACC CCCGACCACAG ACCCGAGTCG GACCTCGGAC AGATGACCTT GAGCGCCTTA TTCTCCAAGG TCCGTCTCCC ACCAATACAC GACATGGGAG
     20           Glyval Lrou lylauva lSe rGlyLeuSer LeuGluProv alTyrTrpAs nSerAlaAsn LysArgPheS lnAlaGlul  yGlyTyrVal LeuTyrProGln

401  AGATGGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGGCCC CCCCGGGCCCC GCCTCCTGGC CTCCTAATTA TGACTTCTAC AAGCTGTACT TGGTAGGCCC
     TCTAGCCCCT GGCCGATCTG GACGAGACGG GGGCCCGGGC CGGAGGACCG GGAGGATTAAT ACTCAAGATG TTCGACATGG ACCATCCCC
     54           IleGlyAs pArgLeuAsp LeuLeuCysP rGlyleuAsn oArgAlaAar gProProGly PraHisSerS erProAsnTy rGluPheTyr LysLeuTyrL euValGlyGly

501  TGCTCAGGGC CGGCCCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA CCCGGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAC AGGCCTGGAG
     ACGAGTCCCG GCCGCGACAC TCCGTGGGGG ACGGGGTTTG GAGGAAGAGT CAACACTAGC GGGTCTGGAC CTAGAGGCGA AGTGGTAGTT CAAGGTCCTC TCGGACGTCC
     87           AlaGlnGly ArgArgCysG luAlaProFr oAlaProAsn LeuLeuLeuT hrCysAspAr gProAspleu AspLeuArgP heThrIleLy sPheGlnGlu SerLeuGlnGly

601  TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA CTTCTCGCACC AGTGGGGACAA TCCTTCTCCC AGTCCCCGAG GGGCCTGGAG AGGCCTGCAGGA
     ATATCGGGAT TAGAGACCCC GGTGCTCAAG GCGAGCGTGG TGCTAATGAT GTAGTAACGG TCAGGAGGCTC TCACCCTGTT CTCCCGACA TCGGGACGTCC
     120          TyrSerProA snLeuTrpgl yHisSerHis ArgSerHisR rIleIleAla isAspTyrTy rIleIleAla ThrSerAspG lyGlyValVa lGlyLeuGlu SerLeuGlnGly

701  GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCC AGTGGGACAA AGTCCCCGAG GAGGGGCTCT CCCCCGAAAA CCCCACCAGC AATGCAACCT CCCGGGGTGC
     CTCCACACAC GGATTGGTCT CCGTACTTCC ACGAAGAGGC TCACCCTGTT TCAGGGGCTC CTCCCCGACA GGGGCTTTT GGGGTGGTCC ACGGTGGGGTCC
     154          GlyValCy   sLeuThrArg GlyMetLysV alLeuLeuAr gValGlyGlu  lyGlyAlaVa  ThrSerAspG   lyLeuLeuGlu  iProArggl   SerLeuLeuGlu luMetProMet

801  CGAAAGAGAC CGAGGGGGCAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC TGCCAGGTCA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC
     CCTTCTCTG GCTCCCCGTC GGGTGTCGGA TTCCTCTTGG TTCCTCCACT ACGGTGGGTCC GGGTGGGTCG TTACGTTGGA GGGCCCCCACG ACTTCGGGGG
     187          GluArgAsp ArgGlyAlaA laHisSerLe uGluProGly LysGluAsnL euProGlyAs pProThrSer AsnAlaThrS erArgGlyAl aGluGlyPro

901  CTGCCCCCCC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GCGGGCTGCC GCTGCTCTTC CTGGCCATG GGTGCCATG TGTTGCCGGA
     GACGGGGGG GTCGTACGG ACGTCACCGA CXXCGTGGTC CCCCGACGG GGACGAGAAC CCACGGTAC GGTGCCATG AGAAGGCGT
     220          LeuProProp roSerMetPr oAlaValAla GlyAlaAlaC lyGlyLeuAl aLeuLeuLeu LeuGlyLeuL laGlyAlaGl yGlyAlaMet yGlyGlyGlyM

1001 GACGGGAGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC CGGAGGGGAG GGTCTCCTGG CCTGGGGGGT CCTGGGGGGT
     CTGCCCCCCG GTTCGGAAGC CTCTCAGCGG TGGACCAGG ACCGAGGAAG CCTCCCCCTC CCAGAGACCC GGACCCCCCA CCTKACCCT ACCCTGGAAC
     254          ArgArgAl  aLysProSer GluSerArgH isProGlyPr oGlySerPhe GlyArgGlyC lySerLeuL yLeuSerLeu lySerLeul yLeuGlyGlyL GlyGlyGlyM etGlyProArg
```

FIGURE 2B

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1101 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGGT GGCGGGGCTG CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTCAGTGG TGACTATGGG
     CCTCCGACTC GGACCCCTCG ATCCCTATCG AGACGCCCCA CCGCCCCGAC GTCTAGGGGG GAAGACGGGG GTGATACTCT TCCACTCACC ACTGATACCC
287  GluAlaGlu  ProGlyGluL euGlyIleAl aLeuArgGly GlyGlyAlaA laAspProPr oPheCysPro HisTyrGluL ysValSerGl yAspTyrGly

1201 CATCCCTGT ATATCGTGCA GGATGGGCCC CTCCAAACAT CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC
     GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GAGGTTTGTA GATGATGTTC CATACTCCCG AGGAGAGTGC ACCGATAGGA CTTAGGTCGG
320  HisProValT yrIleValGl nAspGlyPro ProGlnSerP roProAsnIl eTyrTyrLys ValOP*

1301 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA ACATCTCGGC CCCCTCTGCC CCCCAGCCC CTTCACTCCT CCCGGCTGCT
     GAAGAACCCC ACGAGGAGGT CAAATTAAGG ACCAAACTCC CTGTGGAGAT TGTAGAGCCG GGGGTCGGG GAAGTGAGGA GGGCCGACGA

1401 GTCCCTGTCT CCACTTTTAG GATTCCTTAG GATTCCCACT GCCCCCACTC CTGCCCCTCC GTTTGGCCAT GGGTGCCCCC CTCTCTCTCA GTGTCCCTGG
     CAGGAGCAGA GGTGAAATTC CTAAGGAATC CTAAGGGTGA CGGGGGAGGG CAAAACCGTA CCCACGGGGG GAGACAGAGT CACAGGGACC

1501 ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG ACCCAGCCAT CCTTGTCCCC CAGAGCTAGG GGCGGGAACA
     TAGGAAAAAG GAACCCCTCC CCGTGTCCGA GTCGGAGTAG AGACTGGTAC TGGGTCCGTA GGAACAGGGG GTCTCGATCC CCGCCCCTTGT

1601 GCCCACCTT TGGTTGGCAC CGCCTTCTTT CTGGTTTTCT CTTCTTCTATC TCTTATTCTT CCGTCTCTAG GTCTGTTCTT
     CGGGTGGAAA ACCAACCGTG GCGGAAGAGT GACGGAGAGT GACCAAAAGA GAAGAGATAG AGAATAAGAA AGGGAGAGAA GGCAGAGATC CAGACAAGAA

1701 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTTCTCCC
     GAAGGGATCG TAGGGAGGAG GGTGTAGAGG AAAGTGGGAG AACCGAAGAA TAGGACACGG AGAGGGTAGA GGACCCACCC CCCTAGTTTC GTAAAGAGGG

1801 CTTAGCTTTC AGCCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCCTCAG ATGGGGGCCT TATGGGGAAG GCTCCTGACAC TCCACCCCAG
     GAATCGAAAG TCGGGGGGAA GACTGGAGAG TATGGTTGCT CAGGGGAGTC TACCCCCGGA ATACCCCTTC CGAGACTGTG AGGTGGGGTC

1901 CTCAGGCCAT GGGCACCAGG GCTCCATTCT CTGGGCCTGGC ACATACTTAC CCAGGCCATT TGGGGTGGT GGGTCATGAC AGCTACCATG
     GAGTCCGGTA CCCGTCGTCC CGAGGTAAGA GACCGGACCG GGTCCGGAGA TGTATGAATG AGGTCGGTAA ACCCCACCAA CCCAGTACTG TCGATGGTAC

2001 AGAAGAAGTG TCCCGTTTTC TCCAGTGGCC AATAGCAAGA TATGAACCGG TCGGGGACATG GTCTCATGCT GGGTCATGGCCA CTTGGGACCG
     TCTTCTTCAC AGGGCAAAAC AGGTCACCGG TTATCGTTCT ATACTTGGCC AGCCCTGTAC CAGACTACGA CTTACCCGGT GAACCCTGGC

2101 GAACTGACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCATCCAG
     CTTCACTGAA CGAGGTCTGT TCTCCACTGG TCCGGGGCCTG TCTTTACCGG ACCCTTCATC GTCTTCGTCA CGTCGTCCTT GACCTTCACG GAAGTAGTC

2201 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA GTGGCTTAGT CTGGGGGATC AGGAGGTCGG AGTGGGATGG TTCTTATTCT
     CTGTCCTTCA TCGTGAAGAC TTTGTCCTTC ACCAGACCGA CCTTGAGGTT CACCGAATCA GACCCCCTAG TCCTCCACCC TCACCCTACC AAGAATAAGA

2301 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACTT ACTGACTGTA AGAGGTTAGA GGTGGACCGA
     CACCTCTTCT TCCCGCCCTT CTTGAAGGAA AGTCCTCCTT CGACCTTGAA TGACTGACAT TCTCCAATCT CCACCTGGCT
```

FIGURE 3A

AL-2b.L 1189 TGGTGACTA ● GCATCC TGTGTATA CGTGCAGGATG ● CCCCCCAGA

AL-2b.L 1239 GCCCTCCAAACATCTACTACACATCGATT CTGTGTTGGAGTGGCCCATA

AL-2b.L 1289 TTGCAT CGATACAACTGTT TTCATGCGATCCAAGTGCTGCCGTGTCAC

AL-2b.L 1339 TACATTC TATT CCTGTGCAAGTTATTACGACATCGACTTGCCGGATGA

AL-2b.L 1389 CTTCATTTAGCTTTACGACCCTGAACCCATCCATGCAGGCCTGCAGAGCA

AL-2b.L 1439 CAGATGGGGGAATTCCGGAATCAGATGGTGTT TCTGGGGGGACAGGATCCT

AL-2b.L 1489 GGGTACGGCTC TGTTTGTGCTTGTGCTTATTCTTCTTCTTGGGAGGCTGA

AL-2b.L 1539 ATATGCATCAGACGACAGTGCTCCGGCAACGGGCCAGTGTGGAGGCGGAA

AL-2b.L 1589 GCCGGCCAGCATGGTCCCCTGTGATAGGATTGAAAGAGCTACTGAGAATA

AL-2b.L 1639 GGGGCCTTCTCAATGAGAGAGCGCAGGCTGCTGTTATCATGGGAACCAGG

AL-2b.L 1689 CAGATCAATCATCCCTGGCAGGTCAGGCAGGAAGTTACTTAGCTTCTCCT

AL-2b.L 1739 TCACCTTCTTCCCACAGAATTTATTATAGGCTTGTTCCAAG TGTAGTGT

AL-2b.L 1789 GTGATCAGATTCGT GCTGCCTGTCAGCTCTGTGCTACC GGCAGTTCCCC

AL-2b.L 1839 TCATGGAATTCGATATCAAGCTTATCGATACCGTCGACCT

FIGURE 3B

lerk2   1   MA.RPGQRW..WL.VAMVVWALCRLATPLAKNLEFVSW.NPKFLSGKG
huHTKL   1   MAVRRDSVWKYCWGVLMV...LCRTAISKSIVLEFIYWKSSVSKFLPGQG
AL2.sht   1   VG..PPHSGPGGVRVGALLLLGVLGLVSGL..SLEPVYWNSANKRFQAEGG
AL2.long 1   VG..PPHSGPGGVRVGALLLLGVLGLVSGL..SLEPVYWNSANKRFQAEGS

lerk2   50 .VIYPKIGDKLDIICPRA...EAGR..PYEYYKLYLVRPEQAAACSTVLD
huHTKL   48 LVLYPQIGDKLDIICPKV...DSKTVGQYEYYKVYMVCKDQADRCT..KKE
AL2.sht   48 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long 49 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAQGRRCEAPPA

lerk2   95 PNVLVTCNAPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYIITSTNGSLEG
huHTKL   95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFKNKDYYIISTSNGSLEG
AL2.sht   98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long 96 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2   145 LENREGGVCRTRTMKILMKVCGDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL   145 LDNQEGGVCQTRAMKILMKVGQCASS.....AGSTRNKCPTRRPELEAG
AL2.sht   148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVEEMPMERDRGAAHSLE
AL2.long 148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVGEMPMERDRGAAHSLE

lerk2   195 APGSRGSLQDSDGKHETVNQEEKSGPGASGGSGDPQGFFNSKVALFAAV
huHTKL   199 TNG.RSSTTSPFVKPNPGSSTDGNSAGHSG......NNILGSEVALFAGI
AL2.sht   198 .PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL...ALLLLGVA
AL2.long 198 .PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL...ALLLLGVA

lerk2   245 GAGCVIFLLIIFLTVLLKLRKRHRKHTQ.QRAAALSLSTLASPKGGSG
huHTKL   233 ASGCIIFIVIIITLVVLLKYRRRHRKHSP.GHTTLSLSTLAITPKRSGN
AL2.sht   244 GAGGA....MCWRRRAKPSEERHPGPGSFGRGGSLGLGG....GGGMG
AL2.long 244 GAGGA....MCWRRRAKPSESRHPGPGSFGRGGSLGLGG....GGGMG

lerk2   294 TAGTEPSDIIIPLR...TTENNYCPHYEKVSGCYGHPVYIVQEMPPQSPA
huHTKL   281 NNGSEPSDIIIPLR...TADSVFCPHYEKVSGCYGHPVYIVQEMPPQSPA
AL2.sht   285 PREAEPGELGIALRGGGAADPPFCPHYEKVSGCYGHPVYIVQDGPPQSPP
AL2.long 285 PREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQGPP

lerk2   341 NIYY...
huHTKL   328 NIYY...
AL2.sht   335 NIYY...
AL2.long 335 NIYYTSISVLEWPILHTIQLFFNRSKCSRVTTFLFPVQVITTSTCRMTSF

lerk2   343 ....KV..............
huHTKL   332 ....KV..............
AL2.sht   335 ....KV..............
AL2.long 385 SFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVIILLLGRLNMH

AL2.long 435 CTTLLRDRASVEAEAGQHGPL

FIGURE 4

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LERK2.1    1  M A · R P G Q R · · · K W L V A M V V W A L C R L A T P L A K N L E P V S W S L N P K F L S G K G
huHTKL     1  M A V R R D S V W K Y C W G V L M V · · · L C R T A I S K S I V L E P I Y W N S S N S K F L P G Q G
ALII.long  1  M G P P H S G P · G G V R V G A L L L · · L G V L G L V S G L S L E P V Y W N S A N K R F Q A E G G

LERK2.1   50  L V I Y P K I G D K L D I I C P R A · · · E A G R · · P Y E Y Y K L Y L V R P E Q A A C S T V L D
huHTKL    48  L V L Y P Q I G D K L D I I C P K V · · · D S K T V G Q Y E Y Y K V Y M V D K D Q A D R C T I K K E
ALII.long 48  Y V L Y P Q I G D R L D L L C P R A R P P G P H S S P N Y E F Y K L Y L V G G A Q G R R C E A P P A

LERK2.1   95  P N V L V T C N R P E Q E I R F T I K F Q E F S P N Y M G L E F K K H H D Y Y I T S T S N G S L E G
huHTKL    95  N T P L L N C A K P D Q D I K F T I K F Q E F S P N L W G L E F Q K N K D Y Y I I S T S N G S L E G
ALII.long 98  P N L L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H H D Y Y I I A T S D G T R E G

LERK2.1  145  L E N R E G G V C R T R T M K I I M K V G Q D P N A V T P E Q L T T S R P S K E A D N T V K M A T Q
huHTKL   145  L D N Q E G G V C Q T R A M K I L M K V G Q D A S S · · · · · · A G S T R N K D P T R R P E L E A G
ALII.long148  L E S L Q G G V C L T R G M K V L L R V G Q S P R · · · · · · · G G A V P R K P V S E M P M E · R

LERK2.1  195  A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL   189  T N G · R S S T T S P F V K P N P G S S T D G N S A G H S G · · · · · N N I L G S E V A L F A G I
ALII.long189  D R G A A H S L E P G K E N L P G D P T S N A T S R G A E G · · · · · · P L P P P S M P A V A G A

LERK2.1  245  G A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q Q R A A A L S L · · · S T L A S P K G G
huHTKL   232  A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P Q H T T T L S L · · · S T L A T P K R S
ALII.long232  A G G L A L L L L G V A G A G G A M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G G G

LERK2.1  292  S · G T A G T E P S D I I I P L R · · · T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q
huHTKL   279  G · N N N G S E P S D I I I P L R · · · T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q
ALII.long282  G M G P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q

LERK2.1  338  S P A N I Y Y · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · ·
huHTKL   325  S P A N I Y Y · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · ·
ALII.long332  S P P N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M

LERK2.1  345  · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · K V · · · · · · · · · · · · · ·
huHTKL   332  · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · K V · · · · · · · · · · · · · ·
ALII.long382  T S F S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L

ALII.long432  N M H Q T T L L R Q R A S V E A E A G Q H G P L
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FIGURE 5